

SEQUENCE LISTING



<110> Hilton, Douglas J.
Nicola, Nicos A.
Farley, Alison
Wilson, Tracy
Zhang, Jian-Guo
Alexander, Warren
Rakar, Steven
Fabri, Louis
Kojima, Tetsuo
Maeda, Masatsugu
Kikuchi, Yasufumi
Nash, Andrew

<120> A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

<130> DAVIES COLLISON CAVE (CIP)

<140> 09/037,657

<141> 1998-03-10

<150> 08/928,720

<151> 1997-09-11

<160> 54

<170> PatentIn Ver. 2.0

<210> 1

<211> 5

<212> PRT

<213> Unknown

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<223> Description of Unknown Organism: haemopoietin receptor

<220>

<221> UNSURE

<222> (3)

<223> Unsure at position 3

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<210> 2

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: M116 probe

<400> 2
actcgctcca gattcccgcc tttt 24

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:M108 probe

<400> 3
tcccgccttt ttcgacccat agat 24

<210> 4
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<400> 4
ggtacttggc ttggaagagg aaat 24

<210> 5
<211> 24
<212> DNA
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<400> 5
cggctcacgt gcacgtcggg tggg 24

<210> 6
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<400> 6
agctgctgtt aaagggcttc tc 22

<210> 7
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<212> DNA
<213> Unknown

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<221> unsure
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<220>
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<400> 7
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15

<210> 8
<211> 15
<212> DNA
<213> Unknown

<220>
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<400> 8
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15

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:1944 probe

<400> 9
aagtgtgacc atcatgtgga c 21

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 10
ggaggtgtta aggaggcg 18

<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 11
atgcccgcgg gtcgcccg 18

<210> 12
<211> 1629
<212> DNA
<213> Unknown

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<222> (124)..(1362)

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ccccgcagac tcgccccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120

ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 168
Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
1 5 10 15

ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
20 25 30

ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 264
Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
35 40 45

ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
 50 55 60

tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
 65 70 75

acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 80 85 90 95

acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
 Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 100 105 110

cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 115 120 125

gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
 130 135 140

atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 145 150 155

ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
 160 165 170 175

C! tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
 180 185 190

act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
 195 200 205

act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca 792
 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
 210 215 220

aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac 840
 Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
 225 230 235

ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag 888
 Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
 240 245 250 255

ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc 936
 Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
 260 265 270

caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg 984

Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	
			275					280					285			
aag	gtg	gtg	gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	1032
Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	
		290					295					300				
ctg	aag	ccc	ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	1080
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	
	305					310					315					
ggg	atc	tat	ggg	tcg	aaa	aag	gcg	gga	atc	tgg	agc	gag	tgg	agc	cac	1128
Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	
320					325					330					335	
ccc	acc	gct	gcc	tcc	acc	cct	cga	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	1176
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly	
				340					345					350		
ggg	gtg	tgc	gag	ccg	cgg	ggc	ggc	gag	ccc	agc	tcg	ggc	ccg	gtg	cgg	1224
Gly	Val	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	
			355					360					365			
cgc	gag	ctc	aag	cag	ttc	ctc	ggc	tgg	ctc	aag	aag	cac	gca	tac	tgc	1272
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	
		370					375					380				
tcg	aac	ctt	agt	ttc	cgc	ctg	tac	gac	cag	tgg	cgt	gct	tgg	atg	cag	1320
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	
	385					390					395					
aag	tca	cac	aag	acc	cga	aac	cag	gtc	ctg	ccg	gct	aaa	ctc			1362
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	Val	Leu	Pro	Ala	Lys	Leu			
400					405				410							
taaggatagg	ccatcctcct	gctgggtcag	acctggaggc	tcacctgaat	tggagcccct											1422
ctgtaccatc	tgggcaacaa	agaaacctac	cagaggctgg	ggcacaatga	gctcccacaa											1482
ccacagcttt	ggtccacatg	atggtcacac	ttggatatac	cccagtgtgg	gtaaggttgg											1542
ggtattgcag	ggcctcccaa	caatctcttt	aaataaataa	aggagttggt	caggtaaaaa											1602
aaaaaaaaaa	aaaaaaaaaa	aaaaaaa														1629

<210> 13
 <211> 413
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Murine NR6.1

<400> 13
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Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
 20 25 30
 Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
 50 55 60
 Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
 65 70 75 80
 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
 85 90 95
 Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
 100 105 110
 Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
 115 120 125
 Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
 130 135 140
 Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
 145 150 155 160
 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
 165 170 175
 Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
 180 185 190
 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
 195 200 205
 Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
 210 215 220
 Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
 225 230 235 240
 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
 245 250 255
 Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
 260 265 270
 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
 275 280 285
 Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
 290 295 300
 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
 305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
340 345 350

Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
405 410

<210> 14
<211> 1673
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (125)..(1399)

<220>
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ccccgcagac tcgccccgcg ccataccgg cgttgagtc accgcccgtt gcgcgccacc 120

ccca atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 169
Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
1 5 10 15

ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 217
Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
20 25 30

ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 265
Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
35 40 45

ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 313
Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
50 55 60

tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 361
Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
65 70 75

acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 409

Thr 80	Leu	Asn	Gly	Arg	Arg 85	Leu	Pro	Ser	Glu	Leu 90	Ser	Arg	Leu	Leu	Asn 95	
acc	tcc	acc	ctg	gcc	ctg	gcc	ctg	gct	aac	ctt	aat	ggg	tcc	agg	cag	457
Thr	Ser	Thr	Leu	Ala 100	Leu	Ala	Leu	Ala	Asn 105	Leu	Asn	Gly	Ser	Arg 110	Gln	
cag	tca	gga	gac	aat	ctg	gtg	tgt	cac	gcc	cga	gac	ggc	agc	att	ctg	505
Gln	Ser	Gly	Asp 115	Asn	Leu	Val	Cys	His 120	Ala	Arg	Asp	Gly	Ser 125	Ile	Leu	
gct	ggc	tcc	tgc	ctc	tat	gtt	ggc	ttg	ccc	cct	gag	aag	ccc	ttt	aac	553
Ala	Gly	Ser 130	Cys	Leu	Tyr	Val	Gly 135	Leu	Pro	Pro	Glu	Lys 140	Pro	Phe	Asn	
atc	agc	tgc	tgg	tcc	cgg	aac	atg	aag	gat	ctc	acg	tgc	cgc	tgg	aca	601
Ile	Ser 145	Cys	Trp	Ser	Arg	Asn 150	Met	Lys	Asp	Leu	Thr 155	Cys	Arg	Trp	Thr	
cgc	ggt	gca	cac	ggg	gag	aca	ttc	tta	cat	acc	aac	tac	tcc	ctc	aag	649
Pro	Gly	Ala	His	Gly 160	Glu 165	Thr	Phe	Leu	His 170	Thr	Asn	Tyr	Ser	Leu	Lys 175	
tac	aag	ctg	agg	tgg	tac	ggt	cag	gat	aac	aca	tgt	gag	gag	tac	cac	697
Tyr	Lys	Leu	Arg 180	Trp	Tyr	Gly	Gln	Asp 185	Asn	Thr	Cys	Glu	Glu	Tyr 190	His	
act	gtg	ggc	cct	cac	tca	tgc	cat	atc	ccc	aag	gac	ctg	gcc	ctc	ttc	745
Thr	Val	Gly 195	Pro	His	Ser	Cys	His 200	Ile	Pro	Lys	Asp	Leu 205	Ala	Leu	Phe	
act	ccc	tat	gag	atc	tgg	gtg	gaa	gcc	acc	aat	cgc	cta	ggc	tca	gca	793
Thr	Pro	Tyr 210	Glu	Ile	Trp	Val	Glu 215	Ala	Thr	Asn	Arg	Leu 220	Gly	Ser	Ala	
aga	tct	gat	gtc	ctc	aca	ctg	gat	gtc	ctg	gac	gtg	gtg	acc	acg	gac	841
Arg	Ser 225	Asp	Val	Leu	Thr	Leu 230	Asp	Val	Leu	Asp 235	Val	Val	Thr	Thr	Asp	
ccc	cca	ccc	gac	gtg	cac	gtg	agc	cgc	gtt	ggg	ggc	ctg	gag	gac	cag	889
Pro	Pro	Pro	Asp 240	Val	His 245	Val	Ser	Arg	Val 250	Gly	Gly	Leu	Glu	Asp	Gln 255	
ctg	agt	gtg	cgc	tgg	gtc	tca	cca	cca	gct	ctc	aag	gat	ttc	ctc	ttc	937
Leu	Ser	Val	Arg 260	Trp	Val	Ser	Pro	Pro	Ala 265	Leu	Lys	Asp	Phe	Leu 270	Phe	
caa	gcc	aag	tac	cag	atc	cgc	tac	cgc	gtg	gag	gac	agc	gtg	gac	tgg	985
Gln	Ala	Lys 275	Tyr	Gln	Ile	Arg	Tyr 280	Arg	Val	Glu	Asp	Ser 285	Val	Asp	Trp	
aag	gtg	gtg	gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	1033
Lys	Val 290	Val	Asp	Asp	Val	Ser	Asn 295	Gln	Thr	Ser	Cys	Arg 300	Leu	Ala	Gly	
ctg	aag	ccc	ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	1081
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	

305	310	315	
ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His 320 325 330 335			1129
ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly 340 345 350			1177
ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg 355 360 365			1225
cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys 370 375 380			1273
tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln 385 390 395			1321
aag tca cac aag acc cga aac cag gac gag ggg atc ctg cct tcg ggc Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly 400 405 410 415			1369
aga cgg ggt gcg gcg aga ggt cct gcc ggt taaactctaa ggataggcca Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly 420 425			1419
tcctcctgct gggtcagacc tggaggctca cctgaattgg agcccctctg taccatctgg			1479
gcaacaaaga aacctaccag aggctggggc acaatgagct cccacaacca cagctttgggt			1539
ccacatgatg gtcacacttg gatatacccc agtgtgggta aggttgggggt attgcagggc			1599
ctcccaacaa tctcttttaa taaataaagg agttgttcag gtaaaaaaaaa aaaaaaaaaa			1659
aaaaaaaaaa aaaa			1673

<210> 15
 <211> 425
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Murine NR6.2

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 20 25 30
 Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro

35					40					45					
Gln	Asp	Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	Ser
50						55					60				
Ile	His	Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	Thr
65					70					75					80
Leu	Asn	Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	Thr
				85					90					95	
Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	Gln
			100					105					110		
Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	Ala
		115					120					125			
Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	Ile
130					135						140				
Ser	Cys	Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro
145					150					155					160
Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr
				165					170					175	
Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr
			180					185					190		
Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr
		195					200					205			
Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg
	210					215					220				
Ser	Asp	Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro
225					230					235					240
Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu
				245					250					255	
Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln
			260					265					270		
Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys
		275					280					285			
Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu
	290					295					300				
Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly
305					310					315					320
Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	Pro
				325					330					335	
Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly	Gly

	340		345		350										
Val	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	Arg
	355						360					365			
Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	Ser
370						375					380				
Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	Lys
385					390					395					400
Ser	His	Lys	Thr	Arg	Asn	Gln	Asp	Glu	Gly	Ile	Leu	Pro	Ser	Gly	Arg
				405					410					415	
Arg	Gly	Ala	Ala	Arg	Gly	Pro	Ala	Gly							
			420					425							

<210> 16
 <211> 938
 <212> DNA
 <213> Unknown

<220>
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 <222> (1)..(465)

<220>
 <223> Description of Unknown Organism: Murine NR6.3

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Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
1 5 10 15	
ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac ccc acc gct	96
Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala	
20 25 30	
gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc ggg gtg tgc	144
Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys	
35 40 45	
gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg cgc gag ctc	192
Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu	
50 55 60	
aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc tcg aac ctt	240
Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu	
65 70 75 80	
agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag aag tca cac	288
Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His	
85 90 95	
aag acc cga aac cag gta gga aag ttg ggg gag gct tgc gtg ggg ggt	336
Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly	

100 105 110
 aaa gga gca gag gaa gag aga gac ccg ggt gag cag cct cca caa cac 384
 Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
 115 120 125
 cgc act ctt ctt tcc aag cac agg acg agg gga tcc tgc cct cgg gca 432
 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
 130 135 140
 gac ggg gtg cgg cga gag gta agg ggg tct ggg tgagtggggc ctacagcagt 485
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
 145 150 155
 ctagatgagg ccctttcccc tccttcgggtg ttgctcaaag ggatctctta gtgctcattt 545
 caccactgc aaagagcccc aggttttact gcatcatcaa gttgctgaag ggtccaggct 605
 taatgtggcc tcttttctgc cctcagggtcc tgccggctaa actctaagga taggccatcc 665
 tcctgctggg tcagacctgg aggcacacct gaattggagc ccctctgtac ctatctgggc 725
 aacaaagaaa cctaccatga ggctggggca caatgagctc ccacaaccac agctttgggc 785
 cacatgatgg tcacacttgg atatacccca gtgtgggtaa ggttggggta ttgcagggcc 845
 tcccaacaat ctcttttaaat aaataaagga gttgttcagg taaaaaaaaa aaaaaaaaaa 905
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 938

<210> 17
 <211> 155
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Murine NR6.3

<400> 17
 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 1 5 10 15
 Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
 20 25 30
 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
 35 40 45
 Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
 50 55 60
 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65 70 75 80
 Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
 85 90 95

Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
 100 105 110
 Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
 115 120 125
 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
 130 135 140
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
 145 150 155

<210> 18
 <211> 834
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(834)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence of products generated by 5' RACE of brain
 cDNA using NR6 specific primers

<400> 18
 ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc tct ata cat 48
 Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
 1 5 10 15
 gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg acc ctc aat 96
 Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
 20 25 30
 ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac acc tcc acc 144
 Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
 35 40 45
 ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag cag tca gga 192
 Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
 50 55 60
 gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg gct ggc tcc 240
 Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
 65 70 75 80
 tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac atc agc tgc 288
 Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
 85 90 95
 tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca ccg ggt gca 336
 Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
 100 105 110
 cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag tac aag ctg 384

His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu		
		115					120					125					
agg	tgg	tac	ggg	cag	gat	aac	aca	tgt	gag	gag	tac	cac	act	gtg	ggg	432	
Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly		
	130					135					140						
ccc	cac	tca	tgc	cat	atc	ccc	aag	gac	ctg	gcc	ctc	ttc	act	ccc	tat	480	
Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr		
	145				150					155					160		
gag	atc	tgg	gtg	gaa	gcc	acc	aat	cgc	cta	ggc	tca	gca	aga	tct	gat	528	
Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp		
				165					170					175			
gtc	ctc	aca	ctg	gat	gtc	ctg	gac	gtg	gtg	acc	acg	gac	ccc	cca	ccc	576	
Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro		
			180					185					190				
gac	gtg	cac	gtg	agc	cgc	gtt	ggg	ggc	ctg	gag	gac	cag	ctg	agt	gtg	624	
Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val		
		195					200					205					
cgc	tgg	gtc	tca	cca	cca	gct	ctc	aag	gat	ttc	ctc	ttc	caa	gcc	aag	672	
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys		
	210					215					220						
tac	cag	atc	cgc	tac	cgc	gtg	gag	gac	agc	gtg	gac	tgg	aag	gtg	gtg	720	
Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val		
	225				230					235				240			
gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	ctg	aag	ccc	768	
Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro		
				245					250					255			
ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	ggg	atc	tat	816	
Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr		
			260					265					270				
ggg	tcg	aaa	aag	gcg	gga											834	
Gly	Ser	Lys	Lys	Ala	Gly												
		275															

<210> 19

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Haemopoietin receptor

<400> 19

Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	Ser	Ile	His
1				5					10					15	

Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	Thr	Leu	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	Thr	Ser	Thr
		35					40					45			
Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	Gln	Ser	Gly
	50					55					60				
Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	Ala	Gly	Ser
65					70					75					80
Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Cys
				85					90					95	
Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala
			100					105					110		
His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu
		115					120					125			
Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly
	130					135					140				
Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr
145					150					155					160
Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp
				165					170					175	
Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro
			180					185					190		
Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val
	195						200					205			
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys
	210					215					220				
Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val
225					230					235					240
Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro
				245					250					255	
Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr
			260					265					270		
Gly	Ser	Lys	Lys	Ala	Gly										
		275													

<210> 20
 <211> 143
 <212> DNA
 <213> Artificial Sequence
 <220>

<221> CDS
<222> (105)..(143)

<220>

<223> Description of Artificial Sequence:Nucleotide
sequence unique to 5' RACE of brain cDNA

<400> 20

ggcatgaagg cttaggggtgg ggatcggtag gacccatgca cccagagaaa gggactggtg 60
gcaactttca aactctctgg ggaaggaaga agggctgaaa gagg atg aac ggg ctc 116
Met Asn Gly Leu
1

aga cac agc tgt aat cag ccc cca gga 143
Arg His Ser Cys Asn Gln Pro Pro Gly
5 10

<210> 21

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence encoded
by Nucleotide sequence unique to 5' RACE of brain cDNA

<400> 21

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
1 5 10

<210> 22

<211> 1930

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:Murine NR6

<400> 22

ggcacgagct tcgctgtccg cgcccagtgga cgcgcggtgcg gacccgagcc ccaatctgca 60
ccccgcagac tcgccccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120
cccaatgccc gcgggtcgcc cgggccccgt cgcccaatcc gcgcggcgcc cgccgcggcc 180
gctgtcctcg ctgtggtcgc ctctgttgct ctgtgtcctc ggggtgcctc ggggcggatc 240
gggagcccac acagctgtaa tcagccccca ggacccacc cttctcatcg gctcctccct 300
gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg ggctctactg 360
gacctcaat ggtcgccgcc tgccctctga gctgtcccgc ctccctaaca cctccaccct 420
ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca atctggtgtg 480

tcacgcccga gacggcagca ttctggctgg ctctgectc tatgttggct tgccccctga 540
 gaagcccttt aacatcagct gctgggtcccga gaacatgaag gatctcacgt gccgctggac 600
 accgggtgca cacggggaga cattcttaca taccaactac tccctcaagt acaagctgag 660
 gtggtacggt caggataaca catgtgagga gtaccacact gtgggccctc actcatgcca 720
 tatccccaag gacctggccc tcttcaactcc ctatgagatc tgggtggaag ccaccaatcg 780
 cctaggctca gcaagatctg atgtcctcac actggatgtc ctggacgtgg tgaccacgga 840
 cccccaccc gacgtgcacg tgagccgcgt tgggggcctg gaggaccagc tgagtgtgcg 900
 ctgggtctca ccaccagctc tcaaggattt cctcttccaa gccaagtacc agatccgcta 960
 ccgcgtggag gacagcgtgg actggaaggt ggtggatgac gtcagcaacc agacctcctg 1020
 ccgtctcgcg ggcctgaagc ccggcacctg ttacttcgtc caagtgcgtt gtaaccatt 1080
 cgggatctat gggctcgaaaa aggcgggaat ctggagcgag tggagccacc ccaccgctgc 1140
 ctccaccct cgaagtgagc gcccgggccc gggcgggcgg gtgtgcgagc cgcggggcgg 1200
 cgagcccagc tcgggcccgg tgccggcgga gctcaagcag ttctcggct ggctcaagaa 1260
 gcacgcatac tgctcgaacc ttagtttccg cctgtacgac cagtggcgtg cttggatgca 1320
 gaagtcacac aagacccgaa accaggtagg aaagttgggg gaggcttgcg tggggggtaa 1380
 aggagcagag gaagagagag acccgggtga gcagcctcca caacaccgca ctcttctttc 1440
 caagcacagg acgaggggat cctgccctcg ggcagacggg gtgcggcgag aggtaagggg 1500
 gtctgggtga gtggggccta cagcagtcta gatgaggccc tttcccctcc ttcggtgttg 1560
 ctcaaaggga tctcttagtg ctcatctcac ccactgcaaa gagccccagg ttttactgca 1620
 tcatcaagtt gctgaagggt ccaggcttaa tgtggcctct tttctgccct caggctcctgc 1680
 cggctaaact ctaaggatag gccatcctcc tgctgggtca gacctggagg ctcacctgaa 1740
 ttggagcccc tctgtacctc tctgggcaac aaagaaacct accatgaggc tggggcacia 1800
 tgagctccca caaccacagc tttgggtccac atgatggtca cacttgata taccacagt 1860
 tgggtaaggt tgggggtattg cagggcctcc caacaatctc tttaaataaa taaaggagtt 1920
 gttcaggtaa 1930

<210> 23
 <211> 560
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence:PCR product for
human NR6

<400> 23

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tccaggcagc ggtcggggga caacctcgtg tgccacgccc gtgacggcag catcctggct 60
ggctcctgcc tctatgttgg cctgccccca gagaaacccg tcaacatcag ctgctgggtcc 120
aagaacatga aggacttgac ctgccgctgg acgccagggg cccacgggga gaccttcctc 180
cacaccaact actccctcaa gtacaagctt aggtggtatg gccaggacaa cacatgtgag 240
gagtaccaca cagtggggcc ccactcctgc cacatcccca aggacctggc tctctttacg 300
ccctatgaga tctgggtgga ggccaccaac cgctggggct ctgcccgctc cgatgtactc 360
acgctggata tcttggtatg ggtgaccacg gacccccgc cgcagctgca cgtgagccgc 420
gtcggggggc tggaggacca gctgagcgtg cgctgggtgt cgccaccgc cctcaaggat 480
ttcctttttc aagccaaata ccagatccgc taccgagtgg aggacagtgt ggaatggaag 540
gtggtggacg atgtgagcaa 560
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<210> 24

<211> 1391

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1) .. (1050)

<220>

<223> Description of Unknown Organism:Nucleotide
sequence of clone HFK-66 encoding human NR6

<400> 24

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acc ctc aac ggg cgc cgc ctg ccc cct gag ctc tcc cgt gta ctc aac 48
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
1 5 10 15

gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat ggg tcc agg cag 96
Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
20 25 30

cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac ggc agc atc ctg 144
Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
35 40 45

gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag aaa ccc gtc aac 192
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
50 55 60

atc agc tgc tgg tcc aag aac atg aag gac ttg acc tgc cgc tgg acg 240
Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
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65						70						75						80	
cca ggg gcc cac ggg gag acc ttc ctc cac acc aac tac tcc ctc aag																	288		
Pro Gly Ala His Gly 85						Glu Thr Phe Leu His 90				Thr Asn Tyr Ser Leu 95									
tac aag ctt agg tgg tat ggc cag gac aac aca tgt gag gag tac cac																	336		
Tyr Lys Leu 100						Trp Tyr Gly Gln Asp 105				Asn Thr Cys Glu 110									
aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac ctg gct ctc ttt																	384		
Thr Val Gly 115						Pro His Ser Cys His 120				Pro Lys Asp Leu 125									
acg ccc tat gag atc tgg gtg gag gcc acc aac cgc ctg ggc tct gcc																	432		
Thr Pro Tyr Glu Ile Trp 130						Val Glu Ala Thr Asn Arg 140													
cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg gtg acc acg gac																	480		
Arg Ser Asp Val Leu 145						Thr Leu Asp Ile Leu 155				Val Val Thr Thr 160									
ccc ccg ccc gac gtg cac gtg agc cgc gtc ggg ggc ctg gag gac cag																	528		
Pro Pro Pro Asp Val 165						His Val Ser Arg Val 170				Gly Gly Leu Glu Asp 175									
ctg agc gtg cgc tgg gtg tgc cca ccc gcc ctc aag gat ttc ctc ttt																	576		
Leu Ser Val 180						Trp Val Ser Pro 185				Ala Leu Lys Asp 190									
caa gcc aaa tac cag atc cgc tac cga gtg gag gac agt gtg gac tgg																	624		
Gln Ala Lys 195						Tyr Gln Ile Arg Tyr 200				Arg Val Glu Asp 205									
aag gtg gtg gac gat gtg agc aac cag acc tcc tgc cgc ctg gcc ggc																	672		
Lys Val Val Asp Asp 210						Val Ser Asn Gln Thr Ser 220				Cys Arg Leu Ala Gly									
ctg aaa ccc ggc acc gtg tac ttc gtg caa gtg cgc tgc aac ccc ttt																	720		
Leu Lys Pro Gly Thr 225						Val Tyr Phe Val Gln 235				Val Arg Cys Asn Pro 240									
ggc atc tat ggc tcc aag aaa gcc ggg atc tgg agt gag tgg agc cac																	768		
Gly Ile Tyr Gly Ser 245						Lys Lys Ala Gly Ile Trp 250				Ser Glu Trp Ser 255									
ccc aca gcc gcc tcc act ccc cgc agt gag cgc ccg ggc ccg ggc ggc																	816		
Pro Thr Ala 260						Ser Thr Pro Arg Ser 265				Glu Arg Pro Gly 270									
ggg gcg tgc gaa ccg cgg ggc gga gag ccg agc tgc ggg ccg gtg cgg																	864		
Gly Ala Cys 275						Glu Pro Arg Gly Glu 280				Pro Ser Ser Gly 285									
cgc gag ctc aag cag ttc ctg ggc tgg ctc aag aag cac gcg tac tgc																	912		
Arg Glu Leu Lys Gln 290						Phe Leu Gly Trp Leu Lys 300				Lys His Ala Tyr Cys									

tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga gcc tgg atg cag 960
 Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
 305 310 315 320

aag tcg cac aag acc cgc aac cag cac agg acg agg gga tcc tgc cct 1008
 Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
 325 330 335

cgg gca gac ggg gca cgg cga gag gtc ctg cca gat aag ctg 1050
 Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
 340 345 350

taggggctca ggccaccctc cctgccacgt ggagacgcag aggccgaacc caaactgggg 1110

ccacctctgt accctcactt cagggcacct gagccctca gcaggagctg ggggtggcccc 1170

tgagctccaa cggccataac agctctgact cccacgtgag gccacctttg ggtgcacccc 1230

agtgggtgtg tgtgtgtgtg tgagggttgg ttgagttgcc tagaaccct gccagggctg 1290

ggggtgagaa ggggagtcac tactcccat tacctagggc ccctccaaaa gagtcctttt 1350

aaataaatga gctatttagg tgcaaaaaaa aaaaaaaaaa a 1391

<210> 25
 <211> 350
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Haemopoietin receptor

<400> 25
 Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1 5 10 15

Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 20 25 30

Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 35 40 45

Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
 50 55 60

Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 65 70 75 80

Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
 85 90 95

Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
 100 105 110

Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
 115 120 125

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:LP1
Oligonucleotide

<400> 27
ttgctcacat cgtccaccac cttc

24

<210> 28
<211> 6663
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6 gene

<400> 28
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ggtaatgaga ccctgtcaag aaaagaaaag aaataaagag acaagaaaat gtttataggc 120
tgtgagacag cttggtgggt aaggggcact tgcctccaat caagatgacc tcagcccat 180
ccctaggaat ccatggtaga aggagaaagc aaactcgcag ctgctgacct ccatacatgt 240
gctccaatgt gcacacacac agggagacat aatcaattaa taggatgtat ttgcttagat 300
ttgagtaggc atttatgact gatgttttaa aatttttatt tgattttatg aaaatataacc 360
tgtttgtatt tggtttggtt tggtttgagt tttgtttatt tgagacaggg cttctctgtg 420
tagtcttggc tgtccttgga actcactctg tagaccaggc tggccttgaa ctcagaaatc 480
cgcttgcttg tgcttcccaa gtgcttagat taaagggtgtg cactgccatt cagcaaaatt 540
gcatacttta accccagtat ttgggaggca gaggcagact aatgtgtgaa ttccaggcta 600
gccaaggata cagagtgaga ccctattctt accctcccc cccaaaacc caaatgtat 660
tttgtgcttg tgtatgtaca tgtgtgttgc agcacgtaaa tgtccaagga caacttgtag 720
aagttctctc cgttcacagt ctaagtctg aattcaaact aaggtcctca ggcttagcca 780
cagtcttctt tatgtactga gccatttcac tggccctgga ttgactgatg aattaatttt 840
tgagataagg tctctttagtag ctctagctag gctcaaacta tgaactccca aggtcatctt 900
gagctgctgg tactcttgct tccaccccaa gtgggtggaat gatactcagg cagcacttct 960
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 35 40 45
 Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser
 50 55 60
 Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly

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Cys Trp Ser Arg Asn Met Lys Asp	Leu Thr Cys Arg Trp Thr	Pro Gly	
	100	105	110
Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser	Leu Lys Tyr Lys		
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Leu Arg Leu Val Arg Ser Glu Xaa His Met Xaa Gly Val Pro His Cys			
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Glu Pro Ser Leu Met Pro Tyr Pro Gln Gly Pro Gly Pro Leu His Ser			
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 ggggtggggg ga 11832

<210> 39
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Murine peptide

<400> 39
 Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln
 1 5 10 15
 Ala Thr Cys Ser Ile His Gly Asp Thr Pro
 20 25

<210> 40
 <211> 21
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 40
 gtccaagtgc gttgtaaccc a 21

<210> 41
 <211> 24
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 41
 gctgagtgtg cgctgggtct cacc 24

<210> 42

<211> 18
<212> DNA
<213> Oligonucleotide Sequence

<400> 42
ggctccactc gctccaga

18

<210> 43
<211> 2079
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (513)..(1775)

<220>
<223> Description of Unknown Organism: Nucleotide Sequence of NR6

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tttttgaaaag ctagctgact cactgttcaa gaaaggagaa cactttcaat tatgctgttt 120

gactgcagtg tcagggatcc aaaggaaatg actccatccc ttccctttca tcccaacctc 180

agtgacagca aattctgatg tgactgaggg ttggcttggtg aaggagtcatt taggaaattc 240

tgccctaagcc atagcgcgat gagaaggatg taccctatgg tgggtgatttt cctgtgcccc 300

ctcagaggaa agttgtcaga tgagcaggtg gagtattcta tagcaaacag caagctaata 360

ggttacacag ataactctct gactttgcct tacagaacct gtgctattga ccttagggca 420

aggttcatgc tcagggggcc aactctgtgg gttaggattt gagtttaagc agcttctgct 480

catatttcag cgcccccgcc agcgccggcc cc atg ccc gcc gcc gcc cgc cgg gcc 533

Met Pro Ala Gly Arg Arg Gly
1 5

ccc gcc gcc caa tcc gcg cgg cgg ccg ccg ccg ttg ctg ccc ctg ctg 581

Pro Ala Ala Gln Ser Ala Arg Arg Pro Pro Pro Leu Leu Pro Leu Leu
10 15 20

ctg ctc tgc gtc ctc ggg gcg ccg cga gcc gga tca gga gcc cac aca 629

Leu	Leu	Cys	Val	Leu	Gly	Ala	Pro	Arg	Ala	Gly	Ser	Gly	Ala	His	Thr		
	25					30					35						
gct	gtg	atc	agt	ccc	cag	gat	ccc	acg	ctt	ctc	atc	ggc	tcc	tcc	ctg	677	
Ala	Val	Ile	Ser	Pro	Gln	Asp	Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu		
	40				45					50					55		
ctg	gcc	acc	tgc	tca	gtg	cac	gga	gac	cca	cca	gga	gcc	acc	gcc	gag	725	
Leu	Ala	Thr	Cys	Ser	Val	His	Gly	Asp	Pro	Pro	Gly	Ala	Thr	Ala	Glu		
				60					65					70			
ggc	ctc	tac	tgg	acc	ctc	aat	ggg	cgc	cgc	ctg	ccc	cct	gag	ctc	tcc	773	
Gly	Leu	Tyr	Trp	Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Pro	Glu	Leu	Ser		
			75					80					85				
cgt	gta	ctc	aac	gcc	tcc	acc	ttg	gct	ctg	gcc	ctg	gcc	aac	ctc	aat	821	
Arg	Val	Leu	Asn	Ala	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn		
		90					95					100					
ggg	tcc	agg	cag	cgg	tcg	ggg	gac	aac	ctc	gtg	tgc	cac	gcc	cgt	gac	869	
Gly	Ser	Arg	Gln	Arg	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp		
	105					110					115						
ggc	agc	atc	ctg	gct	ggc	tcc	tgc	ctc	tat	gtt	ggc	ctg	ccc	cca	gag	917	
Gly	Ser	Ile	Leu	Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu		
	120				125					130					135		
aaa	ccc	gtc	aac	atc	agc	tgc	tgg	tcc	aag	aac	atg	aag	gac	ttg	acc	965	
Lys	Pro	Val	Asn	Ile	Ser	Cys	Trp	Ser	Lys	Asn	Met	Lys	Asp	Leu	Thr		
			140						145					150			
tgc	cgc	tgg	acg	cca	ggg	gcc	cac	ggg	gag	acc	ttc	ctc	cac	acc	aac	1013	
Cys	Arg	Trp	Thr	Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn		
			155					160					165				
tac	tcc	ctc	aag	tac	aag	ctt	agg	tgg	tat	ggc	cag	gac	aac	aca	tgt	1061	
Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys		
		170					175					180					
gag	gag	tac	cac	aca	gtg	ggg	ccc	cac	tcc	tgc	cac	atc	ccc	aag	gac	1109	
Glu	Glu	Tyr	His	Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp		
	185					190					195						
ctg	gct	ctc	ttt	acg	ccc	tat	gag	atc	tgg	gtg	gag	gcc	acc	aac	cgc	1157	
Leu	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg		
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ctg ggc tct gcc cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg	1205
Leu Gly Ser Ala Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val	
220 225 230	
gtg acc acg gac ccc ccg ccc gac gtg cac gtg agc cgc gtc ggg ggc	1253
Val Thr Thr Asp Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly	
235 240 245	
ctg gag gac cag ctg agc gtg cgc tgg gtg tcg cca ccc gcc ctc aag	1301
Leu Glu Asp Gln Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys	
250 255 260	
gat ttc ctc ttt caa gcc aaa tac cag atc cgc tac cga gtg gag gac	1349
Asp Phe Leu Phe Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp	
265 270 275	
agt gtg gac tgg aag gtg gtg gac gat gtg agc aac cag acc tcc tgc	1397
Ser Val Asp Trp Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys	
280 285 290 295	
cgc ctg gcc ggc ctg aaa ccc ggc acc gtg tac ttc gtg caa gtg cgc	1445
Arg Leu Ala Gly Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg	
300 305 310	
tgc aac ccc ttt ggc atc tat ggc tcc aag aaa gcc ggg atc tgg agt	1493
Cys Asn Pro Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser	
315 320 325	
gag tgg agc cac ccc aca gcc gcc tcc act ccc cgc agt gag cgc ccg	1541
Glu Trp Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro	
330 335 340	
ggc ccg ggc ggc ggg gcg tgc gaa ccg cgg ggc gga gag ccg agc tcg	1589
Gly Pro Gly Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser	
345 350 355	
ggg ccg gtg cgg cgc gag ctc aag cag ttc ctg ggc tgg ctc aag aag	1637
Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys	
360 365 370 375	
cac gcg tac tgc tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga	1685
His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg	
380 385 390	
gcc tgg atg cag aag tcg cac aag acc cgc aac cag gac gag ggg atc	1733
Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile	

395	400	405	
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Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro Ala Arg			
410	415	420	
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atcc			2079

Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Val	Asn	Ile	Ser	Cys	Trp	Ser	130	135	140
Lys	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala	His	Gly	145	150	155
Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	Arg	Trp	165	170	175
Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly	Pro	His	180	185	190
Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile	195	200	205
Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp	Val	Leu	210	215	220
Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro	Asp	Val	225	230	235
His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val	Arg	Trp	245	250	255
Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys	Tyr	Gln	260	265	270
Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val	Asp	Asp	275	280	285
Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro	Gly	Thr	290	295	300
Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr	Gly	Ser	305	310	315
Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	Pro	Thr	Ala	Ala	Ser	325	330	335
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Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	Arg	Glu	Leu	Lys	Gln	355	360	365
Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	Ser	Asn	Leu	Ser	Phe	370	375	380
Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	Lys	Ser	His	Lys	Thr	385	390	395
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Arg	Gly	Pro	Ala	Arg												420		

<210> 45
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <223> Description of Artificial Sequence: Fwd Primer

 <400> 45
 tgccccca gaaacccgac aac 23

 <210> 46
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Rev Primer

 <400> 46
 cgtgagtaca tcggagcggg cagag 25

 <210> 47
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 47
 tcaggcgcgc cttgccca cagctgtgat c 31

 <210> 48
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 48
 tcagggcgcg ccttatctgg caggacctct 30

 <210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 49
tcaggcgcgc ctgcccgcgc gccgc 25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 50
ataaggcgcgc ccctggcagg acctctcg 28

<210> 51
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 51
tcaggcgcgc cttgccaca cagctgtgat c 31

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 52
tcaggcgcgc cttatctgg caggacctct 30

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 53

tcaggcgcg ctgcccgcg gccgc

25

C⁷
<210> 54

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

<400> 54

ataaggcgcg ccctggcagg acctctcg

28